

SEQUENCE LISTING

<110>	Smit Pott Dhar Gera Rose	er, i iwal rd, (Robe: , Gui	rt J lshai F.											
<120>	Ther	most	able	Reve	erse	Tra	nscr	ipta	ses a	and (Jses	The	reof		
<130>	0942	.504	0001	/RWE,	/AWL										
<140> <141>		•	-	7											
<150> <151>		•	•	6											
<160>	8														
<170>	Pate	ntIn	ver	sion	3.0										
<210><211><212><213>		ney-I	Muri	ne Le	euker	nia '	Virus	5							
<220> <221> <222>		. (21	51)												
<400> atg gg		tct	cat	cat	cat	cat	cat	cat	aat	ato	act	agc	ato	act	4.8
Met Gl											_	_	_		40
ggt gg Gly Gl	_		_				_		_	_	_	_	_		96
atg ac Met Th															144
gag cc Glu Pro 50	o Asp	_							_		_			_	192
gcc tg Ala Tr 65	_	_				_	_	_	_	-	-				240

_	atc Ile			_		_										288
	ccc Pro															336
_	ctg Leu	_	_	_						_						384
_	ccc Pro 130	_			_										cct Pro	432
_	caa Gln	_	_	_		_										480
	gta Val							_	_				_			528
	tgg Trp								_	_		_				576
	cac His	_	_		_				_		_		_	_		624
_	atg Met 210										_			. –		672
	aaa Lys		-			_		_	_							720
_	gac Asp				_			_	_		_		_		_	768
	gac Asp		_	_	_	_					_	_			_	816
	cgg Arg		_						_						_	864
_	aag Lys 290		_			_	_		_	_	_		_			912

	cta Leu		_		_	_				_		_				960
	atg Met		_			_	_		_					_	_	1008
	GJÀ aaa											_	_	_	_	1056
_	gca Ala	_		_						_			_			1104
	ggc Gly 370		_			_	_			_						1152
	act Thr	_		_	_		_		_	_		_		_	_	1200
	ttt Phe	_	_		_	_			_						_	1248
	ctg Leu										_			_		1296
	cca Pro	_	_						_			_	_	_	_	1344
	gcc Ala 450	_	_		_	_	_		_			_		—	cca Pro	1392
	gtc Val															1440
	gat Asp						_			_			_	_	-	1488
	ttg Leu			_		_	_			_		_		_		1536
	gct Ala	_									_				_	1584
ctt	gat	atc	ctg	gcc	gaa	gcc	cac	gga	acc	cga	CCC	gac	cta	acg	gac	1632

Leu	Asp 530	Ile	Leu	Ala	Glu	Ala 535	His	Gly	Thr	Arg	Pro 540	Asp	Leu	Thr	Asp	
_	_				gcc Ala 550	_	_				_				_	1680
					cag Gln										gag Glu	1728
					gct Ala		_	_		_				_	cag Gln	1776
	-	_	_		gca Ala			_	_			_	_	_		1824
_	_			_	tat Tyr	_			_		_		_		_	1872
					ata Ile 630				-	_					_	1920
					aat Asn	_	_			_	_				_	1968
		_			aga Arg		_				_					2016
_			_	_	gag Glu	_	_				_	_	_			2064
				_	atc Ile					_						2112
	_				ccc Pro 710			_				taa				2151
<210 <211 <212 <213	L> 7 2> F	716 PRT	ney-N	ſurir	ie Le	euken	nia V	/irus	3							
-400) > 2)														

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys His Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr

Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala

His 625	Ile	His	Gly	Glu	Ile 630	Tyr	Arg	Arg	Arg	Gly 635	Leu	Leu	Thr	Ser	Glu 640	
Gly	Lys	Glu	Ile	Lys 645	Asn	Lys	Asp	Glu	Ile 650	Leu	Ala	Leu	Leu	Lys 655	Ala	
Leu	Phe	Leu	Pro 660	Lys	Arg	Leu	Ser	Ile 665	Ile	His	Cys	Pro	Gly 670	His	Gln	
Lys	Gly	His 675	Ser	Ala	Glu	Ala	Arg 680	Gly	Asn	Arg	Met	Ala 685	Asp	Gln	Ala	
Ala	Arg 690	Lys	Ala	Ala	Ile	Thr 695	Glu	Asn	Pro	Asp	Thr 700	Ser	Thr	Leu	Leu	
Ile 705	Glu	Asn	Ser	Ser	Pro 710	Asn	Ser	Arg	Leu	Ile 715	Asn					
<210 <211 <212 <213	L> 4 2> 1	3 47 DNA Artii	Eicia	al												
<220)>															
<223	3> (Oligo	onuc	leot	ide t	emp]	late									
<400 gagt		3 agt g	gttt	tgti	cc ca	agtct	gtag	g cag	gtgtg	gtga	atgg	gaag				47
<210 <211 <212 <213	L> : !>]		Eicia	al												
<220)>															
<223	s> (Oligo	onuc]	leot	ide p	orime	er									
<400 cttc		4 tca d	cacao	etge												18
<210 <211 <212 <213	.> 2 !> I	5 21 ONA Arti1	E i cia	al												

620

615

610

<220>

<223> Oligonucleotide primer

<400: gaaga			ctcca	agcca	ag c											21
<210: <211: <212: <213:	> 2 > I	298 ONA	ericl	nia (coli											
<400: agcg			aatta	aatg	cg ag	gttag	getea	a cto	catta	aggc	acco	ccago	gct (ttaca	acttta	60
tgctt	taag	ggc t	cgta	atgti	g to	gtgga	aatt	g tga	agcg	gata	acaa	attt	cac a	acag	gaaaca	120
															cccgg	180
															cctggc	240
gttad	ccca	aac t	taat	cgc	ct to	gcago	cacat	t cc	ccctt	tcg	ccac	gctgo	gcg (taata	agcg	298
<210: <211: <212: <213:	> 1 > [L515 DNA	ney-N	Muri	ne Le	euker	mia ^v	Virus	5							
<220: <221: <222:	> (CDS (1)	. (151	15)												
<400: atg a Met 1	acc	cta			_	_										48
gag d Glu I		_	_							_		_			-	96
gcc t Ala 1												_		_		144
ctg a				_		_										192
tac o Tyr I 65															-	240
aga d	cta	tta	gac	cag	aga	ata	cta	αta	CCC	tac	cag	tee	CCC	taa	aac	288

Arg	Leu	Leu	Asp	Gln 85	Gly	Ile	Leu	Val	Pro 90	Cys	Gln	Ser	Pro	Trp 95	Asn	
_		_			_	_		cca Pro 105						-		336
_	_	-		_	_	_		aag Lys			_					384
								ttg Leu	_				_			432
_				_		_		aag Lys	_	_			_	_	_	480
								ttc Phe								528
	_						_	acc Thr 185			_			_		576
								gat Asp								624
_					_			gac Asp	_		_		_			672
				_	_	_		tct Ser			_	_				720
								Gly 393								768
								aaa Lys 265	_	_	_		_			816
								ctg Leu			_	_				864
								acc Thr								912
								ctc Leu								960

305	310		315	320	320
-	_		aaa acg ggg act Lys Thr Gly Thr 330	_	Leu Phe Asn
Trp Gly Pro	_		caa gaa atc aag Gln Glu Ile Lys		Gln Ala Leu
_			gat ttg act aag Asp Leu Thr Lys 365	Pro Phe Glu	
	Asp Glu Lys		gcc aaa ggt gtc Ala Lys Gly Val 380		
			gcc tac ctg tcc Ala Tyr Leu Ser 395		Lys Lys Leu
			tgc cta cgg atg Cys Leu Arg Met 410		Val Ala Ala
Ile Ala Val 1	_		aag cta acc atg Lys Leu Thr Met		Gly Gln Pro
_			gag gca cta gtc Glu Ala Leu Val 445	Lys Gln Pro	
Pro Asp Arg 7	Trp Leu Ser	Asn Ala Arg 455	atg act cac tat Met Thr His Tyr 460	Gln Ala Leu	Gln Ala Leu
Leu Leu Asp 7	Thr Asp Arg 470	Val Gln Phe	gga ccg gtg gta Gly Pro Val Val 475	Ala Leu Asn 480	Ala Leu Asn 480
Pro Ala Thr I	Leu Leu Pro 485	Leu Pro Glu	gaa ggg ctg caa Glu Gly Leu Gln 490	His Asn Cys 495	His Asn Cys 495
ctt gat aat t Leu Asp Asn S	_			1519	151

<210> 8

<211> 504

<212> PRT

<213> Moloney-Murine Leukemia Virus

<400> 8 Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly Thr Arg Ala Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys

Leu Asp Asn Ser Arg Leu Ile Asn